

Lincoln et al. 09/618,178

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- 48. (New) A method of determining both genotype and confidence scores at a genetic locus for a plurality of samples of genetic material obtained from a subject and wherein the plurality of samples have been prepared under comparable conditions, comprising:
- (a) assembling input signals from each sample in a Euclidean representation;
- (b) determining the initial conditional probability for each input signal in the Euclidean representation for each genotype;
- (c) computing a conditional probability of each genotype for each input signal, and
- (d) determining the genotype and confidence score for each input signal, thus determining the genotype and confidence score at the genetic locus for each sample.
- 49. (New) A method according to claim 48, wherein the input signals are reaction values.
- 50. (New) A method according to claim 48, wherein the Euclidean representation is a two dimensional plot of a first reaction value on the x axis and a second reaction value on the y axis.
- 51. (New) A method according to claim 49, wherein the reaction values are measurements of an optical signal or a digital image intensity value.
- 52. (New) A method according to claim 50, wherein the reaction values are measurements of an optical signal or a digital image intensity value.
- 53. (New) A method according to claim 51, wherein the optical signal is an optical density.
- 54. (New) A method according to claim 52, wherein the optical signal is an optical density.



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- 55. (New) A method according to claim 48, wherein the input signals are a combination of two reaction values.
- 56. (New) A method according to claim 49, wherein the reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, hybridization, allele-specific amplification and a ligase chain reaction.
- 57. (New) A method according to claim 56, wherein the reaction values are obtained by assaying for alleles using genetic bit analysis.
- 58. (New) A method according to claim 50, wherein the reaction values are obtained by assaying for alleles using a method selected from the group consisting of genetic bit analysis, hybridization, allele-specific amplification and a ligase chain reaction.
- 59. (New) A method according to claim 58, wherein the reaction values are obtained by assaying for alleles using genetic bit analysis.
- 60. (New) A method according to claim 48, further comprising detecting the presence of a downward trend in confidence scores over time.
- 61. (New) A method according to claim 60, further comprising triggering an alarm condition upon detecting a statistically significant downward trend in confidence scores over time.
- 62. (New) A method according to claim 49, wherein the reaction values are obtained by assaying for one or more alleles that provide information relating to a trait.



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63. (New) A method according to claim 50, wherein the reaction values are obtained by assaying for one or more alleles that provide information relating to a trait.

64. (New) A method according to claim 49, wherein one or more of the reaction values are obtained by assaying for one or more alleles that provide information pertaining to parentage of the subject.

65. (New) A method according to claim 80, wherein one or more of the reaction values are obtained by assaying for one or more alleles that provide information pertaining to parentage of the subject.

66. (New) A method according to claim 48, wherein more than one genetic loci are analyzed.

67. (New) A method according to claim 49, wherein the reaction values are obtained by assaying for one or more alleles that provide information useful for determining the identity of the subject.

68. (New) A method according to claim 50, wherein the reaction values are obtained by assaying for one or more alleles that provide information useful for determining the identity of the subject.

- 69. (New) A method of determining for a plurality of samples analyzed with comparable biochemistry a genotype and confidence score for the genotype at a locus within genetic material, comprising:
- (a) measuring, under comparable condititions, a first reaction value for each sample, indicative of the presence of a given allele at the locus;